

FIG. 1A

1	ATCCTTGCTGGAGCATTCACTAGGCGAGGCGCTCCATCGGACTCACTAGCCGCACTCATG	60
1	M	1
61	AATCGGCACCATCTGCAGGATCACTTTCTGGAAATAGACAAGAAGAACTGCTGTGTGTTT	120
2	N R H H L Q D H F L E I D K K N C C V F	21
121	CGAGATGACTTCATTGTCAAGGTGTTGCCGCCGGTGTGGGGCTGGAGTTTATCTTCGGG	180
22	R D D F I V K V L P P V L G L E <u>F I F G</u>	41
181	CTTCTGGGCAATGGCCTTGCCCTGTGGATTTTCTGTTCCACCTCAAGTCTGGAAATCC	240
42	<u>L L G N G L A L W I F C F</u> H L K S W K S	61
241	AGCCGGATTTTCTGTTCACCTGGCAGTGGCTGACTTTCTACTGATCATCTGCCTGCCC	300
62	S R <u>I F L F N L A V A D F L L I I C L P</u>	81
301	TTCCTGATGACAACATATGTGAGGCGTTGGGACTGGAAGTTTGGGGACATCCCTTGCCGG	360
82	<u>F L M</u> D N Y V R R W D W K <u>F G D I P C R</u>	101
361	CTGATGCTCTTCATGTTGGCTATGAACGCCAGGGCAGCATCATCTTCCTCACGGTGGTG	420
102	<u>L M L F M L A M N R Q G S I I F L T V V</u>	121
421	GCGGTAGACAGGTATTTCCGGGTGGTCCATCCCCACCACGCCCTGAACAAGATCTCCAAT	480
122	<u>A V</u> D R Y F R V V H P H H A L N K I S N	141
481	CGGACAGCAGCCATCATCTCTTGCCCTTCTGTGGGGCATCACTATTGGCCTGACAGTCCAC	540
142	R T <u>A A I I S C L L W G I T I G L T V H</u>	161
541	CTCCTGAAGAAGAAGATGCCGATCCAGAATGGCGGTGCAAATTTGTGCAGCAGCTTCAGC	600
162	<u>L L</u> K K K M P I Q N G G A N L C S S F S	181
601	ATCTGCCATACCTTCCAGTGGCAGCAAGCCATGTTCTCTGGAGTTCTTCTGCCCTG	660
182	I C H T F Q W H E <u>A M F L L E F F L P L</u>	201
661	GGCATCATCTGTTCTGCTCAGCCAGAATTATCTGGAGCCTGCGGCAGAGACAAATGGAC	720
202	<u>G I I L F C S A</u> R I I W S L R Q R Q M D	221
721	CGGCATGCCAAGATCAAGAGAGCCATCACCTTCATCATGGTGGTGGCCATCGTCTTTGTC	780
222	R H A K I K R <u>A I T F I M V V A I V F V</u>	241
781	ATCTGCTTCCTTCCAGCGTGGTTGTGCGGATCCGCATCTTCTGGCTCCTGCACACTTCG	840
242	<u>I C F L P S V V V</u> R I R I F W L L H T S	261
841	GGCACGCAGAATTGTGAAGTGTACCGCTCGGTGGACCTGGCGTTCTTTTCACTCTCAGC	900
262	G T Q N C E V Y R S V D <u>L A F F I T L S</u>	281
901	TTCACCTACATGAACAGCATGCTGGACCCCGTGGTGTACTACTTCTCCAGCCCATCCTTT	960
282	<u>F T Y M N S M L D P V V Y Y F S</u> S P S F	301

FIG. 2A

		1		50				
HGPRBMY74	(1)	MNRHHLQ	DHFLEIDKKNCCVFRDDFI	IKVLPPVLGLEETFGLLGNGLALW				
HM74	(1)	MNRHHLQ	DHFLEIDKKNCCVFRDDFI	IAKVLPPVLGLEETFGLLGNGLALW				
HM74A	(1)	MNRHHLQ	DHFLEIDKKNCCVFRDDFI	IKVLPPVLGLEETFGLLGNGLALW				
Q9EP66	(1)	---MSKS	DHFLVINGKNCCVFRDENI	IAKVLPPVLGLEETFGLLGNGLALW				
GP31_HUMAN	(1)	-----	MPFPNC	SAPSTVVATAVGVTLGLECGTGLLGNNAVALW				
Q9NQ20	(1)	-----	MPFPNC	SAPSTVVATAVGVTLGLECGTGLLGNNAVALW				
Q9BXC0	(1)	-----	MYNGSCCRTEGDTISQVMP	PELLIMAFVLCALGNGLVALC				
Q9JLS1	(1)	-----	MEHTNC	SAASTVVEITAVGIMLTLECVLGLMGNNAVALW				
		51		100				
HGPRBMY74	(51)	IFCFHLKSWKS	SRITL	LFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPC				
HM74	(51)	IFCFHLKSWKS	SRITL	LFNLAVADFLLIICLPFLMDNYVRRSDWNFGDIPC				
HM74A	(51)	IFCFHLKSWKS	SRITL	LFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPC				
Q9EP66	(48)	IFCFHLKSWKS	SRITL	LFNLAVADFLLIICLPFLTDNYVHNWDWRFEGGIPC				
GP31_HUMAN	(38)	TFLFRVRVWKPYAVY	LENLALADLLAACL	PFLAAEYLSLOAWHLGRVGC				
Q9NQ20	(38)	TFLFRVRVWKPYAVY	LENLALADLLAACL	PFLAAEYLSLOAWHLGRVGC				
Q9BXC0	(39)	GFCFHMKTWKPE	STVYLFNLAVADFL	LMICLPERTDYERRRHAFGDIPC				
Q9JLS1	(38)	TEFYRLKLVWKPYAVY	LENLAVADLLLAT	SVPEFAAEYDKGKTWKGLCHMPC				
		101		150				
HGPRBMY74	(101)	RLVLFMLAMNRQGSII	FLT	VVAVDRYFRVVPHHATNKISNR	TAATISCL			
HM74	(101)	RLVLFMLAMNRQGSII	FLT	VVAVDRYFRVVPHHATNKISNR	TAATISCL			
HM74A	(101)	RLVLFMLAMNRQGSII	FLT	VVAVDRYFRVVPHHATNKISNR	TAATISCL			
Q9EP66	(98)	RLVLFMLAMNRQGSII	FLT	VVAVDRYFRVVPHHATNKISNR	TAATISCE			
GP31_HUMAN	(88)	WALHFLDL	DSR	SVGMAFLAAVAL	DRYLRVVHPR	LRKYNL	SPQAAL	GVSGL
Q9NQ20	(88)	WALHFLDL	DSR	SVGMAFLAAVAL	DRYLRVVHPR	LRKYNL	SPQAAL	GVSGL
Q9BXC0	(89)	RVGLFT	LAMNRAGSIV	FLT	VVAVDRYFRVVPHHATNKISNR	TAATISCT		
Q9JLS1	(88)	QLLFLFLAF	SCGVGVAF	ILMTVAL	DRYLRVVHPR	LRKYNL	SLRAAW	GISSL
		151		200				
HGPRBMY74	(151)	LWGLTITGLTVHLL	KKKMPIQNGG--	ANLCSSFSICHTFOWHEAMFLLEFF				
HM74	(151)	LWGLTITGLTVHLL	KKKLIQNGP--	ANVCISFSICHTFOWHEAMFLLEFF				
HM74A	(151)	LWGLTITGLTVHLL	KKKMPIQNGG--	ANLCSSFSICHTFOWHEAMFLLEFF				
Q9EP66	(148)	LWGLTITGLTVHLL	YTNMMTKNGE--	AYLCSSFSICHTFOWHEAMFLLEFF				
GP31_HUMAN	(138)	VWLLMVAL	TCPGLLISEAAQNSTRCHSEY	SRADGSESTIWOEALSCLOFV				
Q9NQ20	(138)	VWLLMVAL	TCPGLLISEAAQNSTRCHSEY	SRADGSESTIWOEALSCLOFV				
Q9BXC0	(139)	LWALVTL	GTVYLLLENHLCVQET--	AVSCESHIMESANGWHDIMFOLEFF				
Q9JLS1	(138)	HWLLMVAL	TPQNLLTCRTTONSTECPSHYPT	GGTKAATCCQEVLLFELQVL				
		201		250				
HGPRBMY74	(199)	LPLGIILFCSARI	IWSLRQRO--	MDRHAKIKRAITFIMVVAIVFVICFLP				
HM74	(199)	LPLGIILFCSARI	IWSLRQRO--	MDRHAKIKRAITFIMVVAIVFVICFLP				
HM74A	(199)	LPLGIILFCSARI	IWSLRQRO--	MDRHAKIKRAITFIMVVAIVFVICFLP				
Q9EP66	(196)	LPLAAILFCSARI	IWSLRQRO--	MDRHAKIKRAITFIMVVAIVFVICFLP				
GP31_HUMAN	(188)	LPEGLIVFCNAGI	IRALOKRLREPEKOPK	LORAOALVITVVVLFALCFLP				
Q9NQ20	(188)	LPEGLIVFCNAGI	IRALOKRLREPEKOPK	LORAOALVITVVVLFALCFLP				
Q9BXC0	(187)	MPLGIILFCSFKI	IWSLRRQO--	LARQARMKKATRFIMVVAIVFITCYLP				
Q9JLS1	(188)	LPEGLISFCNSGL	IRTLQKRLSESDKOPTIR	RARVIVATMLLTFGLCFLP				

FIG. 2B

		251		300
HGPRBMY74	(247)	SVVRIRIFWLLHTSGTONCEVYRSVDLAFFITLSFTYMNSMLDPVVYYF		
HM74	(247)	SVVRIRIFWLLHTSGTONCEVYRSVDLAFFITLSFTYMNSMLDPVVYYF		
HM74A	(247)	SVVRIRIFWLLHTSGTONCEVYRSVDLAFFITLSFTYMNSMLDPVVYYF		
Q9EP66	(244)	SVAVRIRIFWLLKKYNVRNCDIYSVDLAFFITLSFTYMNSMLDPVVYYF		
GP31_HUMAN	(238)	CFLARVLMHIFONLGSCR--ALC-AVAHTSDVTGSLTYLHSVVNPVVYCF		
Q9NQ20	(238)	CFLARVLMHIFONLGSCR--ALC-AVAHTSDVTGSLTYLHSVVNPVVYCF		
Q9BXC0	(236)	SVSAREYFLWTVPSSACD--P---SVHGALHITLSFTYMNSMLDPVVYYF		
Q9JLS1	(238)	SVLTRVLMHIFQEFKSCS--VQQ-ATMRASDIAGSLTCLHSTLSPATYCF		
		301		350
HGPRBMY74	(297)	SSPSFPNFESTLINRCLQRKMTGEPDNNRSTSVELTGDPN-KTRGAPEAL		
HM74	(297)	SSPSFPNFESTLINRCLQRKMTGEPDNNRSTSVELTGDPN-KTRGAPEAL		
HM74A	(297)	SSPSFPNFESTLINRCLQRKMTGEPDNNRSTSVELTGDPN-KTRGAPEAL		
Q9EP66	(294)	SSPSFPNFESTLINRCLRKKTLGEPDNNRSTSVELTGDPN-TTRSIPGAL		
GP31_HUMAN	(285)	SSPTFRSSYRRVFHTLRGKGQAAEPPDFNERDSYS-----		
Q9NQ20	(285)	SSPTFRSSYRRVFHTLRGKGQAAEPPDFNERDSYS-----		
Q9BXC0	(281)	SSPSFPKIFYNKLIKICSLKPKQPGHSKTORPEEMPTSNLGRRCISVANSE		
Q9JLS1	(285)	SNPAFTHSYRKVLKSLRGRRKAAESPSDNLRDSYS-----		
		351		392
HGPRBMY74	(346)	MANSGEPWSPSYLCPTSNNHSSKKGHCHQEPASLEKQLGCCIE		
HM74	(346)	MANSGEPWSPSYLCPTSNNHSSKKGHCHQEPASLEKQLGCCIE		
HM74A	(346)	MANSGEPWSPSYLCPTSP-----		
Q9EP66	(343)	MADESEPGSPPYLASTSR-----		
GP31_HUMAN	(320)	-----		
Q9NQ20	(320)	-----		
Q9BXC0	(331)	QSQSDGQWDPHIVEWH-----		
Q9JLS1	(320)	-----		

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FIG. 3

D = PF_ls_8.29 7tm_1 PF00001 7 transmembrane receptor (rhodopsin family)

Identical Match = 62 Similar = 175 Total # Of Gaps = 10

Identity: Alignment = 22% Query = 16% Target = 23%

Similarity: Alignment = 63% Query = 46% Target = 64%

QS = 41 QE = 291 TS = 1 TE = 275

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Q      41 GNGLALWIFCFHLKSWKSSRIFLFLNLAVADFLLIICLPFLMDNYVRR--WDWKFGDIPCR
      GN+L++W++C+H +   +++ +F++NLAVAD+L+ + +P+ M   Y+   +W FG++ C+
T      1 GNILVIWVICRHKRMRTPTNYFICNLAVADLLFCLTCPWMLYYFHWGHHHPFGRAMCK

Q      99 LMLFMLAMNRQGSIIFLTVAVDYFRVVHPPHALNKIS-NRTAAIISCLLWGITIGLTV
      +  ++  M+   SI FL++ ++DRY  ++HP ++ ++ +  R A+++++ W + + +++
T      61 IWTFYFYMCCYASIFFLCCISIDRYWAICHPMRYRRRMTRPRHAWVMCLVIWVLAFLWSL

Q     158 HL-LK-KKMPIQNGG-----ANLCSSFSICHT-----FQWHEAMFLEFFLPLGII
      +  +  + +++++   ++ C+ +   ++   +++   +++ F++PL ++
T     121 PPLMFWWCYTHECPNHWNNCNHTWCFIDWPHESSHWWTWWRYYYICSCIVGFYIPLLVM

Q     202 LFCSARIIWSLRQRQM-----DRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLH
      +FC  RI++ L+++ +   R  K  ++A   + VV +VF++C+LP  ++ + +++++
T     181 CFCYCRIYRTLWRHARQMASKMRSRKERKAAKMLCVVVVVFFVCWLPYHIFMF-MDTFC-

Q     257 TSGT--QNCEVYRSVDLAFFITLSFTYMNSMLDPVVY
      ++ +  ++CE+ + ++ A++I++ ++Y N++L+P++Y
T     239 MHWWMCWTCELECVPWAYQICVWLAYVNCCLNPIIY

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FIG. 4

Protein	Genbank/SWI SS-PROT Accession	Identities	Similarities
Human HM74 Protein	P49019	95.9%	97.2%
Human HM74 Splice Variant Protein, HM74A	gi AAW94654	93.5%	93.5%
Mouse Seven Transmembrane Spanning Receptor Protein	Q9EP66	76.2%	80.1%
Human GPR31 Protein	O00270	26.9%	39.6%
Human GPR31 Variant Protein	Q9NQ20	27.1%	39.6%
Human Chemokine Receptor Protein	Q9BXC0	46.9	58.0%
Mouse G-Protein Coupled Receptor Protein	Q9JLS1	26.5%	39.3%

FIG. 5

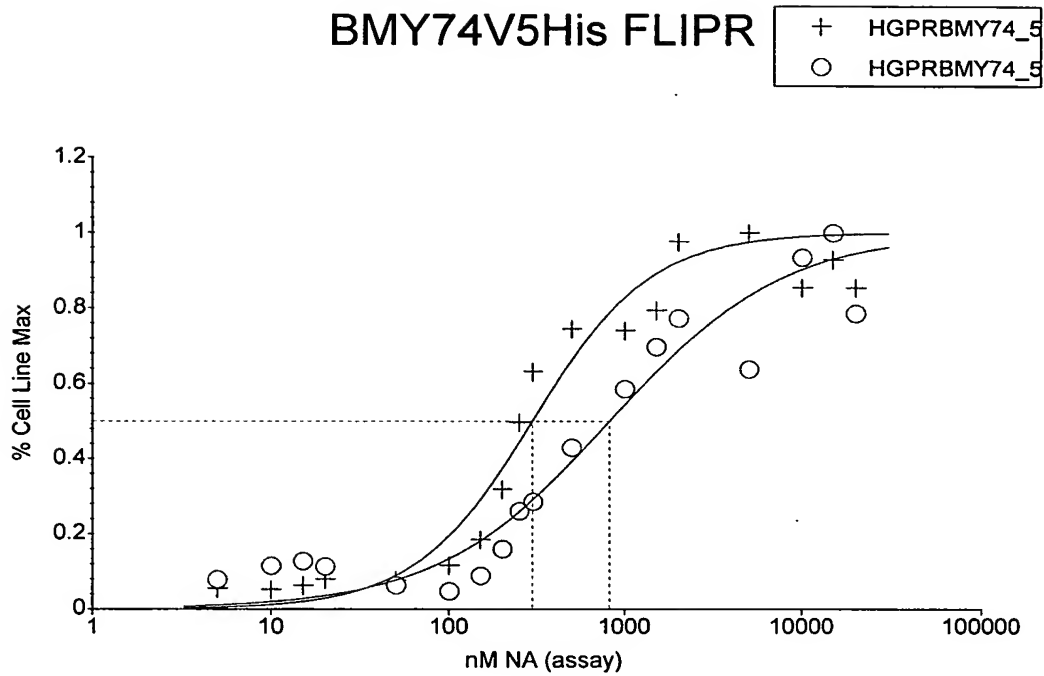


FIG. 6

HM74a vs. HGPRBMV74V5His FLIPR

